

## BLAST

## Basic Local Alignment Search Tool

[NCBI BLAST](#) / [blast help](#) / [Formatting Results](#) - **NXA6CND801S**

gb|U94968.1| (1173 letters)

**Query ID** [align27127310n1384888.110v146334](#)  
**Description** Hordeum vulgare hemoglobin gene, complete cds  
**Molecule type** nucleic acid  
**Query Length** 1173

**Database Name** nr  
**Description** All GenBank+ EMBL+ DDBJ+ PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)  
**Program** BLASTN 2.2.25+

## Descriptions

Legend for links to other resources: [UniGene](#) [GEO](#) [Gene](#) [Structure](#) [Map Viewer](#) [PubChem BioAssay](#)

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
<a href="#">U94968.1</a>	Hordeum vulgare hemoglobin gene, complete cds	2187	2187	100%	0.0	100%	
<a href="#">U91258.1</a>	Hordeum vulgare Harrington haemoglobin apoprotein (hb) mRNA, complete cds	853	1588	73%	0.0	100%	<a href="#">U</a>
<a href="#">HQ390221.1</a>	Triticum aestivum clone UCDA00472 genomic sequence	505	405	29%	3e-109	87%	
<a href="#">DQ345217.1</a>	Zea mays clone 13853 mRNA sequence	578	913	54%	8e-71	98%	<a href="#">U</a>
<a href="#">AF333504.1</a>	Oryza sativa (japonica cultivar-group) hemoglobin 1 (hb1), hemoglobin 3 (hb3), and hemoglobin 4 (hb4) genes, complete cds	244	244	44%	8e-61	76%	<a href="#">G</a>
<a href="#">AC193681.2</a>	Oryza sativa Japonica Group chromosome 3 clone CU1175C11, complete sequence	244	244	44%	8e-61	76%	
<a href="#">AC131596.2</a>	Genomic sequences for Oryza sativa, Nipponbare strain, clone OSJNBa0049C20, from chromosome 3, complete sequence	244	244	44%	8e-61	76%	
<a href="#">U76958.1</a>	Oryza sativa hemoglobin 1 (hb1) gene, complete cds	239	239	44%	4e-59	76%	
<a href="#">AY191386.1</a>	Triticum aestivum cultivar Complet hemoglobin Hb1 mRNA, complete cds	824	817	44%	3e-55	98%	<a href="#">U</a> <a href="#">G</a>
<a href="#">AF281052.1</a>	Zea mays subsp. parviglumis hemoglobin gene, complete cds	185	185	10%	5e-43	94%	
<a href="#">EU186622.1</a>	Zea mays clone 318935 non-symbiotic hemoglobin 2 mRNA, complete cds	180	180	10%	2e-41	93%	<a href="#">U</a> <a href="#">G</a>
<a href="#">EU040115.1</a>	Zea mays full-length cDNA clone ZM_BFc0066D21 mRNA, complete cds	178	178	10%	8e-41	93%	<a href="#">U</a> <a href="#">G</a>
<a href="#">U72644288.1</a>	Zea mays clone 3955 mRNA sequence	178	178	10%	8e-41	93%	<a href="#">U</a>
<a href="#">NM_061114466.1</a>	Zea mays hemoglobin (LOC541815), mRNA >gb AF238080.1 AF238080 Zea mays hemoglobin mRNA, complete cds	178	178	10%	8e-41	93%	<a href="#">U</a> <a href="#">G</a>
<a href="#">AY108330.1</a>	Zea mays P00112753 mRNA sequence	174	174	10%	1e-39	92%	<a href="#">U</a>
<a href="#">AY16618.1</a>	Zea mays hemoglobin gene, complete cds	172	172	10%	4e-39	92%	
<a href="#">EP288488.1</a>	Phyllostachys edulis cDNA clone: bphyem203e02, full insert sequence	162	483	29%	5e-38	98%	
<a href="#">EP101139.1</a>	Phyllostachys edulis cDNA clone: bphyem208d11, full insert sequence	160	483	29%	5e-38	98%	
<a href="#">AG210470.1</a>	Oryza sativa glaberrima clone OG_BB0042C02, complete sequence	139	139	9%	4e-29	88%	
<a href="#">AF338803.1</a>	Oryza sativa (japonica cultivar-group) hemoglobin 2 (hb2) gene, complete cds	139	139	9%	4e-29	88%	<a href="#">G</a>
<a href="#">AC197225.2</a>	Oryza sativa Japonica Group chromosome 3 clone OSJNBa0081P02, complete sequence	139	139	9%	4e-29	88%	
<a href="#">U76028.1</a>	Oryza sativa hemoglobin 2 (hb2) gene, complete cds	132	139	9%	4e-29	88%	
<a href="#">U3468284.1</a>	Oryza rufipogon (W1943) cDNA clone: ORW1943S103H20, full insert sequence	132	132	8%	6e-27	90%	
<a href="#">C1933929.1</a>	Oryza sativa (indica cultivar-group) cDNA clone: OSIGCP1026D01, full insert sequence	132	132	8%	6e-27	90%	<a href="#">U</a>
<a href="#">C1623827.1</a>	Oryza sativa (indica cultivar-group) cDNA	132	132	8%	6e-27	90%	<a href="#">U</a>

	clone:OSIGCP1013P21, full insert sequence						
AE21926.1	Oryza sativa Japonica Group cDNA, clone: J065076013, full insert sequence	132	132	8%	6e-27	90%	
NM_001008872.1	Oryza sativa Japonica Group Os03g0226200 (Os03g0226200) mRNA, complete cds	132	132	8%	6e-27	90%	
AK121522.1	Oryza sativa Japonica Group cDNA clone: J033028N03, full insert sequence	132	132	8%	6e-27	90%	
U75031.1	Oryza sativa hemoglobin 2 mRNA, complete cds	132	132	8%	6e-27	90%	
U001008872.1	Oryza sativa Japonica Group Os03g0233900 (Os03g0233900) mRNA, complete cds	117	119	7%	5e-23	91%	
AK048456.1	Oryza sativa Japonica Group cDNA clone: 001-125-F02, full insert sequence	117	119	7%	5e-23	91%	
U75030.1	Oryza sativa hemoglobin 1 mRNA, complete cds	119	119	7%	5e-23	91%	

## Alignments

**-gb|U94968.1|HVU94968** Hordeum vulgare hemoglobin gene, complete cds  
Length=1173


Score = 2167 bits (1173), Expect = 0.0  
Identities = 1173/1173 (100%), Gaps = 0/1173 (0%)  
Strand=Plus/Plus

Query	1	GAGAACCAAAATTAAAGCGGGAAGGAAGCCATGTCGCCGGAGGGGGCCGTCGTCCTCAG	60
Subject	1	GAGAACCAAAATTAAAGCGGGAAGGAAGCCATGTCGCCGGAGGGGGCCGTCGTCCTCAG	60
Query	61	CGAGGAGAAAGAGGCGCTGCTCAAGTCATGGGCCATCATGAAAGAGGATTCCGCCAA	120
Subject	61	CGAGGAGAAAGAGGCGCTGCTCAAGTCATGGGCCATCATGAAAGAGGATTCCGCCAA	120
Query	121	CCTTGGGCTCCGCTTCTTCTCAAGTACGTACCTGCAATTCCTATTCTATGTGGAAGC	180
Subject	121	CCTTGGGCTCCGCTTCTTCTCAAGTACGTACCTGCAATTCCTATTCTATGTGGAAGC	180
Query	181	AGCGCAATGAAGGCCGCCGATGCATCTCTTGACATGCATGCTGCTGCGTGCCTCCA	240
Subject	181	AGCGCAATGAAGGCCGCCGATGCATCTCTTGACATGCATGCTGCTGCGTGCCTCCA	240
Query	241	GGATCTTCGAGATCGCGCGCTCGCGAGGCAGATGTTCCCGTTCCTCGCGCACTCCGACG	300
Subject	241	GGATCTTCGAGATCGCGCGCTCGCGAGGCAGATGTTCCCGTTCCTCGCGCACTCCGACG	300
Query	301	TGCCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCGGTGTCGCTCTTCGTCATGGTAA	360
Subject	301	TGCCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCGGTGTCGCTCTTCGTCATGGTAA	360
Query	361	TACACCATGCATCTCCCAACGATCTGCTGCTATGCATTACATATATATGCTCCATGGCT	420
Subject	361	TACACCATGCATCTCCCAACGATCTGCTGCTATGCATTACATATATATGCTCCATGGCT	420
Query	421	TATCAATGTGTATGTTGTCGATGAATGTTGCAGACCTCGAGGCGGCTGCGCAGTTGC	480
Subject	421	TATCAATGTGTATGTTGTCGATGAATGTTGCAGACCTCGAGGCGGCTGCGCAGTTGC	480
Query	481	GGAAAGCCGCGCAAGATCACCGTCAGGGAGACCACTGAAAGAGGCTGGGCGGCAACGACT	540
Subject	481	GGAAAGCCGCGCAAGATCACCGTCAGGGAGACCACTGAAAGAGGCTGGGCGGCAACGACT	540
Query	541	TGAAATACGCGCTGCGCAGATGGCCACTTCGAGGTATGCCCACTTGCCCAATTAGCTTGTG	600
Subject	541	TGAAATACGCGCTGCGCAGATGGCCACTTCGAGGTATGCCCACTTGCCCAATTAGCTTGTG	600
Query	601	AATTGTACTAGCATGGGGTGGTGTGATTTTGCAATGCATTCAAAATTTGTCCTCCCTCAC	660
Subject	601	AATTGTACTAGCATGGGGTGGTGTGATTTTGCAATGCATTCAAAATTTGTCCTCCCTCAC	660
Query	661	ACGCTGTGTTCTTCTTCTTCTGCTGTTCACAGGTGACGCGGTTGCTGCTGCTGAGAC	720
Subject	661	ACGCTGTGTTCTTCTTCTTCTGCTGTTCACAGGTGACGCGGTTGCTGCTGCTGAGAC	720
Query	721	GATCAAGAGAGCGCTTCCTCGGCTGACATGTGGGGGCGCCGAGATGAGGAACGCTGGGGCGA	780
Subject	721	GATCAAGAGAGCGCTTCCTCGGCTGACATGTGGGGGCGCCGAGATGAGGAACGCTGGGGCGA	780

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Query 781 GGCATACGATCAACTGGTCTCGGCCATCAAGCAAGAGATGAAGCCAGCTGAGTAGCTCCA 840
Sbjct 781 GGCATACGATCAACTGGTCTCGGCCATCAAGCAAGAGATGAAGCCAGCTGAGTAGCTCCA 840
Query 841 CGGCACCTCATATACCAAGCCATTTTCGCCGATTTGCCGTTCAACCTTCCTTGTCTACCA 900
Sbjct 841 CGGCACCTCATATACCAAGCCATTTTCGCCGATTTGCCGTTCAACCTTCCTTGTCTACCA 900
Query 901 ATTCACTCATTTTCAACCGTTGTGTTTGTATTTGTGTTTATGTGCACATAAAGCTATTATGTA 960
Sbjct 901 ATTCACTCATTTTCAACCGTTGTGTTTGTATTTGTGTTTATGTGCACATAAAGCTATTATGTA 960
Query 961 ACACCTCAATAAAAGTACAAATTTATGCACGATATTACCCCGCTCTACTTTACAGTCTTCT 1020
Sbjct 961 ACACCTCAATAAAAGTACAAATTTATGCACGATATTACCCCGCTCTACTTTACAGTCTTCT 1020
Query 1021 CTCTCTGTAGAGAACTCTGATTAGAGGTTATGCTCTGCTACTAGTACATTGCAATACG 1080
Sbjct 1021 TTTTCTGTAGAGAACTCTGATTAGAGGTTATGCTCTGCTACTAGTACATTGCAATACG 1080
Query 1081 CTTAGAAAAGATGCTTTAAATAAATAAATCAATGTTTTTATAGGCACGCGCTCTATATGTA 1140
Sbjct 1081 CTTAGAAAAGATGCTTTAAATAAATAAATCAATGTTTTTATAGGCACGCGCTCTATATGTA 1140
Query 1141 TCGAGTAAACGTTTAGCCTGTATAAATGAACAC 1173
Sbjct 1141 TCGAGTAAACGTTTAGCCTGTATAAATGAACAC 1173

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>gb|U01228.1|U01228  *Hordeum vulgare* Harrington haemoglobin apoprotein (hb) mRNA,  
complete cds  
Length=939

Sort alignments for this subject sequence by:  
E value    Score    Percent identity  
Query start position    Subject start position

Score = 883 bits (478), Expect = 0.0  
Identities = 481/482 (99%), Gaps = 1/482 (0%)  
Strand=Plus/Plus

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Query 693 AGGTGACGCGGTTCCGCTCTGCTCGAGACGATCAAGGAGGCGCTTCGCGTGACATGTGGG 752
Sbjct 409 AGGTGACGCGGTTCCGCTCTGCTCGAGACGATCAAGGAGGCGCTTCGCGTGACATGTGGG 752
Query 753 GGCOCGAGATGAGGAAACGCTGGGGGCGAGGCATACGATCAACTGGTGGGCCCATCAAGC 812
Sbjct 469 GGCOCGAGATGAGGAAACGCTGGGGGCGAGGCATACGATCAACTGGTGGGCCCATCAAGC 812
Query 813 AAGAGATGAAGCCAGCTGAGTAGTCTCCACCGCACTCATATACCAAGCCATTTTCGCCGAT 872
Sbjct 529 AAGAGATGAAGCCAGCTGAGTAGTCTCCACCGCACTCATATACCAAGCCATTTTCGCCGAT 872
Query 873 TGTCCGTTCAACCTTCCCTCTCTCACCAATTCACCTCATTTTACCGGTTGTGTTTGTATTGT 932
Sbjct 589 TGTCCGTTCAACCTTCCCTCTCTCACCAATTCACCTCATTTTACCGGTTGTGTTTGTATTGT 932
Query 933 GTGTTTATGTGCACTAAAGTCTATTGTAACTCAAT-AAAAGTACAAATTTATGCACGAT 991
Sbjct 649 GTGTTTATGTGCACTAAAGTCTATTGTAACTCAATCAAAGTACAAATTTATGCACGAT 991
Query 992 ATTCACCCCGCTCTACTTTACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1051
Sbjct 709 ATTCACCCCGCTCTACTTTACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 768
Query 1052 TATGCCCTCGTACTAGTACATTGCAATACGCTTAGAAAAGATGCTTTAAATAAATAAATCAA 1111
Sbjct 769 TATGCCCTCGTACTAGTACATTGCAATACGCTTAGAAAAGATGCTTTAAATAAATAAATCAA 828
Query 1112 TGTCTTTTATAGGCACGCGCTGCTTATATGTATCGAGTAAACGTTTATAGCTGTATAAATGAAC 1171
Sbjct 829 TGTCTTTTATAGGCACGCGCTGCTTATATGTATCGAGTAAACGTTTATAGCTGTATAAATGAAC 888
Query 1172 AC 1173
Sbjct 889 AC 890

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Score = 268 bits (145), Expect = 5e-68  
Identities = 145/145 (100%), Gaps = 0/145 (0%)  
Strand=Plus/Plus

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Query 1 GAGAACCAAAATTAAGCGGGAGGAAGCCATGTCTGCCGCGGAGGGGGCGCTGCTCTTCAG 60
Sbjct 35 GAGAACCAAAATTAAGCGGGAGGAAGCCATGTCTGCCGCGGAGGGGGCGCTGCTCTTCAG 94
Query 61 CGAGGAGAAAGGAGGCGCTGCTCAAGTCATGGGCAATCATGAAGAGGATTCGCGCAA 120
Sbjct 95 CGAGGAGAAAGGAGGCGCTGCTCAAGTCATGGGCAATCATGAAGAGGATTCGCGCAA 154
Query 121 CTTTGGGCTCCGCTTCTTCTCTCAAG 145
Sbjct 155 CTTTGGGCTCCGCTTCTTCTCTCAAG 179

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Score = 222 bits (120), Expect = 4e-54  
Identities = 120/120 (100%), Gaps = 0/120 (0%)

Strand=Plus/Plus

Query 455 GACCTGCGAGGCGCGGCTGCGCAGTTGCGGAAAGCGCGCAAGATCACCGTCAGGGAGACACC 514  
 Sbjct 293 GACCTGCGAGGCGCGGCTGCGCAGTTGCGGAAAGCGCGCAAGATCACCGTCAGGGAGACACC 352  
 Query 515 CTTGAAGAGGCTGCGCGGCGCAGCATTGAAATACCGCGTGCAGATGCGCATTGCGAGGT 574  
 Sbjct 353 CTTGAAGAGGCTGCGCGGCGCAGCATTGAAATACCGCGTGCAGATGCGCATTGCGAGGT 412

Score = 213 bits (115), Expect = 2e-51  
 Identities = 120/122 (99%), Gaps = 1/122 (0%)  
 Strand=Plus/Plus

Query 235 CTTCCAGGATCTTCGAGATCGCGCGCTCGGCGAGGCAGATGTTCCGCTTCCTCGCGGACT 294  
 Sbjct 173 CTT-CAAGATCTTCGAGATCGCGCGCTCGGCGAGGCAGATGTTCCGCTTCCTCGCGGACT 231  
 Query 295 CCGACGTGCGCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCGGTGTCCGTCTTCGTCA 354  
 Sbjct 232 CCGACGTGCGCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCGGTGTCCGTCTTCGTCA 291  
 Query 355 TG 356  
 Sbjct 292 TG 293

>gb|HQ390021.1| Triticum aestivum clone UCDA00472 genomic sequence  
 Length=354

Score = 405 bits (219), Expect = 3e-109  
 Identities = 322/366 (88%), Gaps = 30/366 (8%)  
 Strand=Plus/Plus

Query 154 CTGCCATTTCIT--ATT-CTATGTGGAAGCAGCGCAATGAAGCGCGGATGCATCTCCTT 210  
 Sbjct 1 CTGCCATTTCITATATTAC-ATGTAG-AG--GCACATGAAG-CCCGATGCATCTCCTT 55  
 Query 211 GACATGCATGCTGCTGCGGTGCGTGCCTCCAGGATCTTCGAGATCGCGCGCTCGGCGAGGC 270  
 Sbjct 56 GACATGC-TGC-G-TGC-OG-GTGCCTCCAGGATCTTTGAGATCGCGCGCTCGGCGAGGC 110  
 Query 271 AGATGTTCCCGTTCCTGCGCGACTCCGACGTGCGCGTGGAGACCAACCCCAAGCTCAAGA 330  
 Sbjct 111 AGATGTTCCCGTTCCTGCGCGACTCCGACGTGCGCGTGGAGACCAACCCCAAGCTCAAGA 170  
 Query 331 CCCACGCGCGTGTCCGTCTCTCTCATGGTAATACACCATGCATCTCCCAAGCATGCTGCTGC 390  
 Sbjct 171 CCCACGCGCGTGTCCGTCTCTCTCATGGTAATACACCATGCATCTCCCAAGCATGCTACTCC 230  
 Query 391 TATGCATTAC-ATAT--A--TATGCTTCCATGGCTTATCAATGTGTATG-G-T-----GT 438  
 Sbjct 231 TA--G-TTACTATATTTCATATGCTTCCATGGCTGACCAATGTGTATGTGATCCATGT 287  
 Query 439 -T-GCGATGAATGTTGCGACACCTGCGAGGCGCGCTGCGCAGTTGCGGAAAGCGCGCAAGAT 496  
 Sbjct 288 GTTGCATGAATCGCGCAGACGTGCGAGGCGCGCTGCGCAGTTGCGGAAAGCGCGCAAGAT 347  
 Query 497 CACCGT 502  
 Sbjct 348 CACCGT 353

>gb|DQ245217.1| Zea mays clone 13853 mRNA sequence  
 Length=780

Sort alignments for this subject sequence by:  
 E value Score Percent identity  
 Query start position Subject start position

Score = 278 bits (150), Expect = 8e-71  
 Identities = 243/282 (86%), Gaps = 17/282 (6%)  
 Strand=Plus/Plus

Query 693 AGGTGACGCGGTTGCTCTGCTCGAGACGATCAAGGAGGCGCTTCGCGCTGACATGTGGG 752  
 Sbjct 449 AGGTGACGCGGTTGCTCTGCTCGAGACGATCAAGGAGGCGCTTCGCGCGGACATGTGGG 508  
 Query 753 GCGCCGAGATGAGGAACGCGTGGGCGAGGCATACGATCAACTGGTGCAGGCATCAAGC 812  
 Sbjct 509 GCGCCGAGATGAGGAACGCGTGGGCGAGGCATACGACCAACTGGTGCAGGCATCAAGC 568  
 Query 813 AAGAGATGAAGCGAGCTGAGTAGCTCCA-CC---GCATCATAT-A---CCACGCCATT 863  
 Sbjct 569 AAGAGATGAAGCGCCTCTGAGTAGCTC-ATCCATTGTACTCATATCATATGCCACGCAACT 627  
 Query 864 TTGG-CCGATTGCGGTTCGAACTTTCCTGCTTCAACCAATTCACATCATTCACCGT-T-G 920  
 Sbjct 628 TCGGTCC-ATA-TCCGTCCAACTTTCCTGCTTGAACCGGTTCACTCATGTACCATATTG 685  
 Query 921 TTTTGTGATTGTGTGTTTATGTGCACTAAAGTC-TATTGTAA 961  
 Sbjct 686 TTTTGAAGTGTGTGTTTACGTGTACTAAGC-CATATTGTAA 726

Score = 226 bits (122), Expect = 3e-55  
 Identities = 126/128 (99%), Gaps = 0/128 (0%)

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Strand=Plus/Plus
Query 18  GGAAGGAAAGCCATGTCTGCGCGGAGGGGGCCGCTGCTTCACGCGAGGAGGAAGAGGGCGC 77
Sbjct 92  GGAAGGAAAGCCATGTCTGCGCGGAGGGGGCCGCTGCTTCACGCGAGGAGGAAGAGGGCGC 151
Query 78  TGGTGCTCAAGTCATGCGGCCATCATGAAGAAGGATTCGCGCAACCTTGGGCTCCGCTTCT 137
Sbjct 152  TGGTGCTCAAGTCATGCGGCCATCATGAAGAAGGATTCGCGCAACCTTGGGCTCCGCTTCT 211
Query 138  TCTCAAG 145
Sbjct 212  TCTCAAG 219

Score = 213 bits (115), Expect = 2e-51
Identities = 120/122 (99%), Gaps = 1/122 (0%)
Strand=Plus/Plus
Query 235  CCTCCAGGATCTTCGAGATCGCGCCGTGGCGAGGCAGATGTTCCCGTCTCGCGGACT 294
Sbjct 213  CCT-CAAGATCTTCGAGATCGCGCCGTGGCGAGGCAGATGTTCCCGTCTCGCGGACT 271
Query 295  CCGAGCTGCGGCTGGAGACCAACCCCAAGCTCAAGACCCACGCGGTGTCGGCTCTTGGTCA 354
Sbjct 272  CCGAGCTGCGGCTGGAGACCAACCCCAAGCTCAAGACCCACGCGGTGTCGGCTCTTGGTCA 331
Query 355  TG 356
Sbjct 332  TG 333

Score = 195 bits (105), Expect = 8e-46
Identities = 115/120 (96%), Gaps = 0/120 (0%)
Strand=Plus/Plus
Query 455  GACCTGCGAGGCGCGCTGCGCAGTTGCGGAAAGCGCGCAAGATCACCGTCAGGGAGACCAC 514
Sbjct 333  GACGTGCGAGGCTGCTGCGCAGCTGCGGAAAGCGCGCAAGATCACCGTCAGGGAGACCAC 392
Query 515  CCTGAAGAGGCTGGGCGGACGCACTTGAATACGCGGTGGCAGATGGCCACTTCGAGGT 574
Sbjct 393  CCTGAAGAGGCTGGGCGGACGCACTTGAATACGCGGTGGCAGATGGCCACTTCGAGGT 452

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>gb|AF335504.1|  Oryza sativa (japonica cultivar-group) hemoglobin 1 (hbl1), hemoglobin 3 (hb3), and hemoglobin 4 (hb4) genes, complete cds  
Length=11601

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Score = 244 bits (132), Expect = 8e-61
Identities = 62/557 (77%), Gaps = 57/557 (10%)
Strand=Plus/Plus
Query 55  CTTTCAGCGAGGAGAGGAGGCGCTGGTCTCAAGTCATGGGCCATCATGAAGAAGGATTC 114
Sbjct 2410  CTTTCAGCGAGGAGAGGAGGCGCTGGTCTCAAGTCATGGGCCATCATGAAGAAGGATTC 2469
Query 115  CGCCAACTTGGGCTCCGCTCTTCTCTCAAGTACGTACC--C-TG--C--C-ATTTC- 164
Sbjct 2470  CGCCAAATATTGCGCTCCGCTCTTCTCTTGAAGTATGTACATGCGTGTACTACCATTTCTC 2529
Query 165  TATTCTATGTGGAAGCAGCGCAATGAAGCCCGCATGCATCTCC--TTGA-CA-TGCAT-- 219
Sbjct 2530  T-T-T-T-TGCGGAATCAGAG-ATTGG-GTTTGTGAAGCAT-TAAATTGAGCAATGCATTT 2583
Query 220  -GCTG--C-TGCGTG-C-G-T-GCTCC-AGGATCTTCGAGATCGCGCGCTCGCGGAGG 269
Sbjct 2584  CGCTGATACATGTGTCTGATGTGTGTGAGGATCTTCGAGGCTCGCGCGCTCGCGGAGG 2643
Query 270  CAGATGTTCCGCTTCTGCGGCGCATCCGAGCTGCGGCTGGAGAACACCCCAAGCTCAAG 329
Sbjct 2644  CAGATGTTCTCGTTCTGCGCAACTCCGACGTCGCGCTCGAGAGAACCCCAAGCTCAAG 2703
Query 330  ACCCAGCGCGGTGTCCGCTCTTGTGTCATGGTAATAC-ACCATGCATCTCCCAAGATCTGCT 388
Sbjct 2704  ACCCAGCGCATGTCCGCTCTTGTGTCATGGTAATACCATCAT-T--ATT-TCAG-- 2754
Query 389  GCTA-TGCATTACATATA-TATGCTTC-CA-TGGCTTATCAATGTGATG-GTGTGCGA 443
Sbjct 2755  GCAAGTAAATTTGTGTGTA-G-TAGACACTGAC--AG-AATGTGTGCGTGTGCGTGTGGA 2809
Query 444  TGAATGG-T---GCAGACCTGCGAGGCGGCTGCGCGAGTTGCGGAAAGCCGCGAAGTAC 499
Sbjct 2810  TCAATCGATATTGCGAGATGCGAGGCGGCGCGAGCTGCGGAAAGCCGCGAAGTAC 2869
Query 500  CGTCAGGAGACACACCTGAAGAGGCTGGGCGGCGACGCACTTGAATAAGCGGT-GGCAG 558
Sbjct 2870  CGTGAGAGACACACCTCAAGAGGCTCGGCGGCGACGCACTTGAATAAGCGGT-GGCAG 2928
Query 559  ATGGCCACTTCGAGGTA 575
Sbjct 2929  ACGCCCACTTCGAGGTA 2945

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>gb|AC103891.2|  Oryza sativa Japonica Group chromosome 3 clone OJ1175C11, complete sequence  
Length=123620

Score = 244 bits (132), Expect = 8e-61  
 Identities = 425/557 (77%), Gaps = 57/557 (10%)  
 Strand=Plus/Minus

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Query 55      CTTTCAGCGAGGAGAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTC 114
Sbjct 19766   CTTTCAGCGAGGAGAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCTTGAAGAAGGATTC 19707

Query 115     CGCCAAACCTTGGGCTCCGCTTCTCTCTCAAGTACGTACC--C-TG--C-C-ATTCT- 164
Sbjct 19706   CGCCAAATTTGCCCTCCGCTTCTCTCTGAAGTAGTACATGGGTGTACTACCATCTCTC 19647

Query 165     TATTCTATGTGGAAGCAGGCAATGAAGCCCGCATGTCATCTCC-TTGA-CA-TGCAT-- 219
Sbjct 19646   T-TT-T-TGCGGAATCAGAG-ATTGG-GTTTGTGAAGCAT-TAAATTGAGCAATGCATT 19593

Query 220     -GCTG---C-TGCGTG-C-G-T-GCTCC-AGGATCTTCGAGATCGCGCGTGGCGAGG 269
Sbjct 19592   CGCTGATACATGTGTGTCTGATTGTGTGTAGGATCTTCGAGGTGCGCGCTGGCGAGG 19533

Query 270     CAGATGTTCCGCTTCTGCGCACTCCGACGTGCGCGTGGAGACCAACCCCAAGCTCAAG 329
Sbjct 19532   CAGATGTTCTGCTTCTGCGCACTCCGACGTGCGCGTGGAGAAAGACCCCAAGCTCAAG 19473

Query 330     ACCCAACGCGGTGTCGCTCTTGTGTCATGGTAATAC-ACCATGCATCTCCCAACGATCTGCT 388
Sbjct 19472   ACCCAACGCAATGTGCGCTCTTGTGTCATGGTAATACATACCAT-CAT-T---ATT---TCAG-- 19422

Query 389     GCTA-TGCATTACATATA-TATGCTTC-CA-TGGCTTATCAATGTGTATG-TGTGTCCGA 443
Sbjct 19421   CGAAGTAAATTTGTTGTGGTA-G-TAGACACTGAC--AG-AATGTGTGCGTGTGCTCCGGA 19367

Query 444     TGAATGG-T---GCAACCTGCGAGGCGGCTGCGCAGTTGCGGAAAGCCGCGAAGATCAC 499
Sbjct 19366   TCAATCGATATTGCGAGCATGCGAGGCGCGCGCGAGCTGCGGAAAGCCGCGAAGGTAC 19307

Query 500     CGTCAGGGAGACCAACCTGAAGAGGCTGGCGGCGACGCACTTGAATACGCGCT-GCGAG 558
Sbjct 19306   CGTGAAGAGACCAACCTCAAGAGGCTGCGGCGCGACGCACTCAAGTACGCGCTCGG-AG 19248

Query 559     ATGGCCACTTCGAGGTA 575
Sbjct 19247   ACGCCCACTTCGAGGTA 19231
  
```

>gb|AC137696.2| Genomic sequence for *Oryza sativa*, Nipponbare strain, clone OSJNBa0049C20, from chromosome 3, complete sequence  
 Length=136098

Score = 244 bits (132), Expect = 8e-61  
 Identities = 425/557 (77%), Gaps = 57/557 (10%)  
 Strand=Plus/Minus

```

Query 55      CTTTCAGCGAGGAGAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTC 114
Sbjct 131739   CTTTCAGCGAGGAGAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCTTGAAGAAGGATTC 131680

Query 115     CGCCAAACCTTGGGCTCCGCTTCTCTCTCAAGTACGTACC--C-TG--C-C-ATTCT- 164
Sbjct 131679   CGCCAAATTTGCCCTCCGCTTCTCTCTGAAGTATGATACGTGTGTACTACCATTTCTC 131620

Query 165     TATTCTATGTGGAAGCAGGCAATGAAGCCCGCATGTCATCTCC-TTGA-CA-TGCAT-- 219
Sbjct 131619   T-TT-T-TGCGGAATCAGAG-ATTGG-GTTTGTGAAGCAT-TAAATTGAGCAATGCATT 131566

Query 220     -GCTG---C-TGCGTG-C-G-T-GCTCC-AGGATCTTCGAGATCGCGCGTGGCGAGG 269
Sbjct 131565   CGCTGATACATGTGTGTCTGATTGTGTGTAGGATCTTCGAGGTGCGCGCTGGCGAGG 131506

Query 270     CAGATGTTCCGCTTCTGCGCACTCCGACGTGCGCGTGGAGACCAACCCCAAGCTCAAG 329
Sbjct 131505   CAGATGTTCTGCTTCTGCGCACTCCGACGTGCGCGTGGAGAAAGACCCCAAGCTCAAG 131446

Query 330     ACCCAACGCGGTGTCGCTCTTGTGTCATGGTAATAC-ACCATGCATCTCCCAACGATCTGCT 388
Sbjct 131445   ACCCAACGCAATGTGCGCTCTTGTGTCATGGTAATACATACCAT-CAT-T---ATT---TCAG-- 131395

Query 389     GCTA-TGCATTACATATA-TATGCTTC-CA-TGGCTTATCAATGTGTATG-TGTGTCCGA 443
Sbjct 131394   CGAAGTAAATTTGTTGTGGTA-G-TAGACACTGAC--AG-AATGTGTGCGTGTGCTCCGGA 131340

Query 444     TGAATGG-T---GCAACCTGCGAGGCGGCTGCGCAGTTGCGGAAAGCCGCGAAGATCAC 499
Sbjct 131339   TCAATCGATATTGCGAGCATGCGAGGCGCGCGCGAGCTGCGGAAAGCCGCGAAGGTAC 131280

Query 500     CGTCAGGGAGACCAACCTGAAGAGGCTGGCGGCGACGCACTTGAATACGCGGT-GCGAG 558
Sbjct 131279   CGTGAAGAGACCAACCTCAAGAGGCTGCGGCGCGACGCACTCAAGTACGCGCTCGG-AG 131221

Query 559     ATGGCCACTTCGAGGTA 575
Sbjct 131220   ACGCCCACTTCGAGGTA 131204
  
```

>gb|U76029.1|OSU76029 *Oryza sativa* hemoglobin 1 (hbl) gene, complete cds  
 Length=827

Score = 239 bits (129), Expect = 4e-59  
Identities = 424/557 (77%), Gaps = 57/557 (10%)  
Strand=Plus/Plus

Query	55	CTTCACGCGAGGAGAGGAGCGCGTGGTGTCTCAAGTCATGGGCGCATCATGAAGAAGGATTC	114
Sbjct	39	CTTCACGCGAGGAGGAGGAGCGCGTGGTGTCTCAAGTCATGGGCGCATCTTGAAGAAGGATTC	98
Query	115	CGCCCAATCTTGGCGTCCGCTTCTCTCAAGTAGACGCCC—CA—TG—C—A—ATTTC—	164
Sbjct	99	CGCCCAATATTGCCCTCCGCTTCTCTTGAAGTAGATGACATCGSTGTCTTACACCACTTCTC	156
Query	165	TATTCATCTGCGAAGCAGCGCAATTATGGCCCCCGATGCATCTCT—TTGA—CA—TGCAT—	219
Sbjct	159	T—TT—T—TCGCAATACAG—AAT—ATGG—G—TGATCTGGAACAT—TAAATTGACCAATCAATT	212
Query	220	—GCTG—C—TGGCTG—G—G—T—GCTCT—AGGATCTTTCGAGATCGCGCGCTCGCGGAGG	269
Sbjct	213	CGCTGATACATGTGTGTCTGATGTGTGTGTAGCATCTTGTGAGCATCTGCGCGCTCGCGGAGG	272
Query	270	CAGATGTCTCCGCTTCTCGCGAACTCCGACGTGGCGGTGGAGACCAACCCCAAGCTCAAG	329
Sbjct	273	CAGATGTCTCTTCTCGCGAACTCCGACGTGGCGGTGGAGAGAACCCCAAGCTCAAG	332
Query	330	ACCCACGCGCTGTCCCTCTTCCTCATGTGAATAAC—ACCATGCATCTCCCACCATCTCGT	388
Sbjct	333	ACCCACGCGCATCTCCGCTCTTCTGTCATGTGAATAACATACCAT—CAT—T—ATT—TACG—	383
Query	389	GCTA—TGCATTACATATA—TATGCTC—CA—TGGCTTATCATGTGATGTG—GIGTTCGGA—	436
Sbjct	384	GCAAGTAAATTTGTGTGGTA—G—TAGACATGAC—AG—AATGTGTGGTGGGTGGCGA	438
Query	444	TGAATGG—T—CGAGACCTGGGAGCGCGCTGGCGAGTTCGGGAAAGCGGGCAAGATCAC	498
Sbjct	439	TGATTCGATATTGCAGACCTCGAGGCGCCGCGCAGCTGGGAAAGCGGGCAAGGATCAC	493
Query	500	CTCATGAGGAGACCACTCTGAAGAGCTCGGGCGCGGACGCACTCGAAATCGGCT—GGCAG	558
Sbjct	499	CGTGAAGGAGACCACTCAAGAGCTCGGGCGCGCACCACTCAAGATCGGCTCGG—AG	557
Query	559	ATGGCGCATCTTGAGAGTA	575
Sbjct	558	ACGCCCATCTCGAGGTA	574

```
>gb|AY151390.1|  Triticum aestivum cultivar Complet hemoglobin Hb1 mRNA, complete cds
Length=516
```

GENE ID: 543085 LOC543085 | hemoglobin Hb1 [Triticum aestivum]  
(10 or fewer PubMed links)

Sort alignments for this subject sequence by:

E value	Score	Percent identity	Query start position	Subject start position
---------	-------	------------------	----------------------	------------------------

Score = 226 bits (122), Expect = 3e-55  
Identities = 138/146 (95%), Gaps = 0/146 (0%)  
Strand=Plus/Plus

Query	693	AGGTGACGCGGTTCGCTCTGCTCGAGACGATCAAGGAGCGCCTTCGCGGTGACATGTGGG	752
Sbjct	362	AGGTGACGCGGTTCGCTCTGCTCGAGACGATCAAGGAGCGCCTTCGCGGTGACATGTGGG	421
Query	753	GCGCCGAGATGAGGAACCGCTGGGCGAGGACATACGATCAACTGTCGCGGCCATCAAGG	812
Sbjct	422	GCGCCGAGATGAGGAACCGCTGGGCGAGGACATACGATCAACTGTCGCGGCCATCAAGG	481
Query	813	AAGAGATGAAGCCAGCTGAGTAGTCT	838
Sbjct	482	AAGAGATGAAGCCAGCTGAGTAGTCT	507

Score = 213 bits (115), Expect = 2e-51  
Identities = 120/122 (99%), Gaps = 1/122 (0%)  
Strand=Plus/Plus

Query	235	CCTCAGGATCTTCGAGATCGCGCGTGGCGAGGCAGATGTTCCCGTTCCTCGCGGACT	294
Sbjct	126	CTC--CAAGATCTTCGAGATCGCGCGTGGCGAGGCAGATGTTCCCGTTCCTCGCGGACT	184
Query	295	CCTCGACGCGCTGGAGACCAACCCAAAGCTCAAGAGCCACCGCGGTGTCCGCTTCTGTGCA	354
Sbjct	185	CGACGTGCGCGTGGAGACCAACCCAAAGCTCAAGAGCCACCGCGGTGTCCGCTTCTGTGCA	244
Query	355	TG 356	
Sbjct	245	TG 246	

Score = 209 bits (113), Expect = 3e-50  
Identities = 124/129 (97%), Gaps = 1/129 (0%)  
Strand=Plus/Plus

Query 17 GGAAGGAAGCCATGTCTGCCGCGAGGGGGCCGTCGTCTTCAGCGAGGAGAAGGAGGCG 76  
Sbjct 5 GGG-AGGAAGCCATGTCTGCCGCGAGAGAGCCGTCGTGTTTACGCGAGGAGAAGGATGCG 63

```

Query 77 CTGGTGTCTCAAGTCATGGGSCATCATGAAGAAGGATTCGGCCAACTTGGGCTCCGGCTTC 136
Sbjct 64 CTGGTGTCTCAAGTCATGGGSCATCATGAAGAAGGATTCGGCCAACTTGGGCTCCGGCTTC 123

Query 137 TTCTCAAG 145
Sbjct 124 TTCTCAAG 132

```

Score = 167 bits (90), Expect = 2e-37  
 Identities = 110/120 (92%), Gaps = 0/120 (0%)  
 Strand=Plus/Plus

```

Query 455 GACCTGCGAGGCGCGCTGCGCAGTTGCGGAAAGCGGGCAAGATCACCGTCAGGGAGACAC 514
Sbjct 246 GACCTGTCAGGCGCGCGCTGCGCAGTTGCGGAAAGCGGGCAAGATCACCGTCAGGGAGACAC 305

Query 515 CTGAAGAAGGCTGGGCGGACGCACTTTGAAATACGGCTGGCAGATGGCAGCTTCAGGT 574
Sbjct 306 CTGAAGAAGGCTGGGCGGACGCACTTTGAAATACGGCTGGGCGAGATGGCAGCTTTAGGT 365

```

>gb|AF291052.1| Zea mays subsp. parviglumis hemoglobin gene, complete cds  
 length=882

Score = 185 bits (100), Expect = 5e-43  
 Identities = 114/121 (95%), Gaps = 0/121 (0%)  
 Strand=Plus/Plus


```

Query 239 CAGGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGGACTCCGA 298
Sbjct 245 CAGGGTCTTCGAGATCGCGCCGTCGGCGAAGCAGATGTTCTCGTTCCTGCGGACTCCGA 304

Query 299 CGTGCCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCGGTGTCGCTCTTCGTATGGT 358
Sbjct 305 CGTGCCGCTGGAGAAAGAACCCCAAGCTCAAGACCCACGCGATGTTCGCTCTTCGTATGGT 364

Query 359 A 359
Sbjct 365 A 365

```

>gb|EU968226.1|  Zea mays clone 316935 non-symbiotic hemoglobin 2 mRNA, complete cds  
 length=817

GENE ID: 541815 LOC541815 | hemoglobin [Zea mays] (10 or fewer PubMed links)

Score = 180 bits (97), Expect = 2e-41  
 Identities = 114/122 (94%), Gaps = 1/122 (0%)  
 Strand=Plus/Plus


```

Query 235 CUTCAGGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGGACT 294
Sbjct 221 CUTCAGAG-TCTTCGAGATCGCGCCGTCGGCGAAGCAGATGTTCTCGTTCCTGCGGACT 279

Query 295 CCGACGTGCGCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCGGTGTCGCTCTTCGTCA 354
Sbjct 280 CCGACGTGCGCGCTGGAGAAAGAACCCCAAGCTCAAGACCCACGCGATGTTCGCTCTTCGTCA 339

Query 355 TG 356
Sbjct 340 TG 341

```

>gb|BT040115.1|  Zea mays full-length cDNA clone ZM\_BF0066D21 mRNA, complete cds  
 length=760

GENE ID: 541815 LOC541815 | hemoglobin [Zea mays] (10 or fewer PubMed links)

Score = 178 bits (96), Expect = 8e-41  
 Identities = 113/121 (94%), Gaps = 1/121 (0%)  
 Strand=Plus/Plus


```

Query 236 CTCAGGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGGACTC 295
Sbjct 156 CTCAGAG-TCTTCGAGATCGCGCCGTCGGCGAAGCAGATGTTCTCGTTCCTGCGGACTC 214

Query 296 CGACGTGCGCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCGGTGTCGCTCTTCGTCA 355
Sbjct 215 CGACGTGCGCGCTGGAGAAAGAACCCCAAGCTCAAGACCCACGCGCATGTTCGCTCTTCGTCA 274

Query 356 G 356
Sbjct 275 G 275

```

>gb|DQ244258.1|  Zea mays clone 3955 mRNA sequence  
 length=889

Score = 178 bits (96), Expect = 8e-41  
 Identities = 113/121 (94%), Gaps = 1/121 (0%)  
 Strand=Plus/Plus



```

Query 236 CTCAGGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGGACTC 295

```



Shjet	301	CTCAAGG-TCTTCGAGATCGCGCGTTCGGCGAAGCAGATGTTCTCGTCTCCGCGGACTC	359
Query	296	CGACGTGCGCGCTGGAGAACACCCCAAGCTCAAGACCCAGCGGTGTCGTTCTTGGTCAT	358
Shjet	360	CGACGTGCGCGCTGGAGAAAGACCCCAAGCTCAAGACGCACGCCATGTCGTTCTTGGTCAT	419
Query	356	G 356	
Shjet	420	G 420	

```
>ref|NM_001111496.1|  Zea mays hemoglobin (LOC541815), mRNA
gb|AF236080.1|AF236080  Zea mays hemoglobin mRNA, complete cds
length=885
```

```

GENE ID: 541815 LOC541815 | hemoglobin [Zea mays] (10 or fewer PubMed links)
Score = 178 bits (96), Expect = 8e-41
Identities = 113/121 (94%), Gaps = 1/121 (0%)
Strand=Plus/Plus
Query 236 C T C C A G A G A T C T T C G A G A T C G C C C G T C G G C G A G C A G A T G T T C C G C T T C C G G G G A C T C 295
Sbjct 292 C T C A A G G - T C T T C G A G A T C C C C C T C G G C G A A G A C A G A T G T C C G C T T C C G G G G A C T C 350
Query 296 C A G C G T C C C C T C G A G A C A C C C C A A G C T C A A G A C C C A G C C G T C G C G T T C T C G T A T C 355
Sbjct 351 C A G C G T C C C C T T G A G A A A G A C C C A A G C T C A A G A C G C A C C C A T G T C C G T T C T C G T A T 410
Query 356 G 356
Sbjct 411 G 411

```

>gb|AY108330.1|  Zea mays PC0112753 mRNA sequence  
Length=1007

```

Score = 174 bits (94), Expect = 1e-39
Identities = 113/122 (93%), Gaps = 1/122 (0%)
Strand=Plus/Plus

Query 235      CGTCACGAGATCTTCGAGATCGCGCGTGGCGAGGCGAGATGTTCCCGTTCCTGCGCGACT 294
Sbjct 203      CTTCAAGA-TCCTCGATATCGCGTGGCGAGGCGAGATGTTCCGTTCTCGTCGCGACT 341

Query 295      CGCAGCTGCGCTCGAGAGCAACCCCAAGCTCAAGACGACCGCGTCTCCGCTCTGTCTCA 356
Sbjct 342      CGCAGCTGCGCTAGAGAGAAACCCCAAGCTCAAGACGACGCGCATGTCGCTCTGTCTCA 401

Query 355      TG 356
Sbjct 402      TG 403

```

```
>gb|AY005818.1| Zea mays hemoglobin gene, complete cds
Length=874
```

```

Score = 172 bits (93), Expect = 4e-39
Identities = 113/122 (93%), Gaps = 3/122 (2%)
Scrand=Plus/Plus

Query 239 CAGAGATCTTGGAGATCGCGCGCTGGCG-GAGGCAGATGTTCCCGTCTCTGGCGGACTCCG 297
Sbjct 255 CAGG-TCTTGGAGATCGCGCGCTGGCGGCA-CCGATGTTCTCGTCTGGCGGCACTCCG 312
Query 298 ACGTGGCGCTGGAGACCAACCCCAAGCTCAAGACCACGCGCTGTCGGTCTTCGTCATGG 357
Sbjct 313 ACGTGGCGCTAGAGAAAGAACCCCAAGCTCAAGACGCAAGCCATGTGGTCTTCGTCATGG 372

Query 358 TA 359
Sbjct 373 TA 374

```

>emb|FP098496.1| Phyllostachys edulis cDNA clone: bphyem203e02, full insert sequence  
Length=2533

Sort alignments for this subject sequence by:

E value	Score	Percent identity	Query start position	Subject start position
---------	-------	------------------	----------------------	------------------------

```
Score = 169 bits (91), Expect = 5e-38
Identities = 127/144 (89%), Gaps = 4/144 (2%)
Strand=Plus/Minus

Query 693   AGGTGACGGCGTCTGCTCTGCTGAGACGATCAAGGAGGC+GTTCTCCGGCTGACATGTGG   751
Sbjct 2043   AGGTGACAAAGTCTGGCGTCTGTTGACAGCATAAAGGAGGCTG-TTCCGGCTGACATGT-G   2100

Query 752   GGCGCC-GGAGTAGGAGGAGCTGGGGGGGAGGACATAGCATCAACTGGTGGCGGCATCAA   810
Sbjct 2101   GGCGCCGGAGGATGAAGAACGCTTGGGGGAGAGGCTACAGCCACTGTGGCGGCATCAA   2160

Query 811   GCAAGAGATGAAGCGCTGTGAGTA   834
```

Sbjct 2161 GCAAGAGATGAAGCCATCTGGTA 2184

Score = 161 bits (87), Expect = 8e-36  
Identities = 110/121 (91%), Gaps = 2/121 (1%)  
Strand=Plus/Plus

```

Query 455 GACCTGCGAGGCGCGCTGCGCAGTTGCGGAAAGCGGCAAGATCACCGTCAGGGAGACCAC 514
          |||
Sbjct 1927 GACCTGCGAGGCGCGCTGTCGACGCTGCGGAAATCCGCGAGGTCACCGTCAGGGAGACCAC 1986
          |||
Query 515 CTTGAAGAGGCTGGGCGGCAAGCACTTGAATAACGGCGTGGCAGATGGCACT-TCGAGG 573
          |||
Sbjct 1987 CTTGAAGAGGCTGGGCGGCAAGCACTTCAAGTACGGCGTGGCAGATGGCACTAT-GAGG 2045
          |||
Query 574 T 574
          |
Sbjct 2046 T 2046
          |

```

Score = 152 bits (82), Expect = 5e-33  
Identities = 84/85 (99%), Gaps = 0/85 (0%)  
Strand=Plus/Plus

```

Query 55 CTTGAGCGAGGAGAGGAGGCGCTGGTCTCAAGTCATGGGCCATCATGAAGAAGGATTC 114
          |||
Sbjct 1723 CTTGAGCGAGGAGAGGAGGCGCTGGTCTCAAGTCATGGGCCATCATGAAGAAGGATTC 1782
          |||
Query 115 CGCCAACCTTGGGCTCCGCTTCTTC 139
          |||
Sbjct 1783 CGCCAACCTTGGGCTCCGCTTCTTC 1807
          |||

```

>emb|FP101139.1| Phyllostachys edulis cDNA clone: bphym208d11, full insert sequence  
Length=926

Sort alignments for this subject sequence by:  
E value Score Percent identity  
Query start position Subject start position

Score = 169 bits (91), Expect = 5e-38  
Identities = 127/144 (89%), Gaps = 4/144 (2%)  
Strand=Plus/Plus

```

Query 693 AGGTGACGCGGCTTGGCTCTGCTCGAGACGATCAAGGAGGC-GCTTCGGGCTGACATGTGG 751
          |||
Sbjct 457 AGGTGACAAAGTTTGGGCTGCTTGAAGCATTAAGGAGGCTG-TTCGGGCTGACATGT-G 514
          |||
Query 752 GGGCCG-CAGAGTAGAGAAACGCGTGGGCGGAGGCATACGATCAACTGGTCGGGCCATCAA 810
          |||
Sbjct 515 GGGCCGCGAGATGAAGAACGCTTGGGCGGAAGCCTTACGACCACTGGTGGGCCATCAA 574
          |||
Query 811 GCAAGAGATGAAGCCAGCTGAGTA 834
          |||
Sbjct 575 GCAAGAGATGAAGCCATCTGGTA 598
          |||

```

Score = 161 bits (87), Expect = 8e-36  
Identities = 110/121 (91%), Gaps = 2/121 (1%)  
Strand=Plus/Plus

```

Query 455 GACCTGCGAGGCGCGCTGCGCAGTTGCGGAAAGCGGCAAGATCACCGTCAGGGAGACCAC 514
          |||
Sbjct 341 GACCTGCGAGGCGCGCTGTCGACGCTGCGGAAATCCGCGAGGTCACCGTCAGGGAGACCAC 400
          |||
Query 515 CTTGAAGAGGCTGGGCGGCAAGCACTTGAATAACGGCGTGGCAGATGGCACT-TCGAGG 573
          |||
Sbjct 401 CTTGAAGAGGCTGGGCGGCAAGCACTTCAAGTACGGCGTGGCAGATGGCACTAT-GAGG 459
          |||
Query 574 T 574
          |
Sbjct 460 T 460
          |

```

Score = 152 bits (82), Expect = 5e-33  
Identities = 84/85 (99%), Gaps = 0/85 (0%)  
Strand=Plus/Plus

```

Query 55 CTTGAGCGAGGAGAGGAGGCGCTGGTCTCAAGTCATGGGCCATCATGAAGAAGGATTC 114
          |||
Sbjct 137 CTTGAGCGAGGAGAGGAGGCGCTGGTCTCAAGTCATGGGCCATCATGAAGAAGGATTC 196
          |||
Query 115 CGCCAACCTTGGGCTCCGCTTCTTC 139
          |||
Sbjct 197 CGCCAACCTTGGGCTCCGCTTCTTC 221
          |||

```

>gb|AC210470.1| Oryza glaberrima clone OG\_BB0042002, complete sequence  
Length=128640


Score = 139 bits (75), Expect = 4e-29  
Identities = 103/116 (89%), Gaps = 4/116 (3%)  
Strand=Plus/Minus

```

Query 39 CGGAGGGG-GCGGTC-GTCTTCAGCGAGGAGAGGCGCTGGTCTCAAGTCATGGGC 96
          |||
Sbjct 20311 CGG-GGGAGCGGTCAG-CTTCAGCGAGGAGAGGAGGCGCTGGTCTCAAGTCGTTGGC 20254
          |||

```

Query 97 CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTCTCAAGTACGTAC 152  
 Sbjct 20253 CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTCTGAAGTATGTAC 20198

**>gb|AF335503.1|**  Oryza sativa (japonica cultivar-group) hemoglobin 2 (hb2) gene, complete cds  
 Length=3793

GENE ID: 4332123 Os03g0226200 | Os03g0226200 [Oryza sativa Japonica Group]  
 (10 or fewer PubMed links)

Score = 139 bits (75), Expect = 4e-29  
 Identities = 103/116 (89%), Gaps = 4/116 (3%)  
 Strand=Plus/Plus

Query 39 CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGGAGGCGCTGGTCTCAAGTCATGGGC 96  
 Sbjct 992 CGG-GGGGAGCGGTTCAG-CTTCAGCGAGGAGCAGGAGGCGCTTGTGCTCAAGTCGTGGGC 1049  
 Query 97 CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTCTCAAGTACGTAC 152  
 Sbjct 1050 CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTCTGAAGTATGTAC 1105

**>gb|AC107226.2|**  Oryza sativa Japonica Group chromosome 3 clone OSJNBa0081F02, complete sequence  
 Length=162425

Score = 139 bits (75), Expect = 4e-29  
 Identities = 103/116 (89%), Gaps = 4/116 (3%)  
 Strand=Plus/Minus

Query 39 CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGGAGGCGCTGGTCTCAAGTCATGGGC 96  
 Sbjct 137007 CGG-GGGGAGCGGTTCAG-CTTCAGCGAGGAGCAGGAGGCGCTTGTGCTCAAGTCGTGGGC 136950  
 Query 97 CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTCTCAAGTACGTAC 152  
 Sbjct 136949 CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTCTGAAGTATGTAC 136894

**>gb|U76028.1|OSU76028** Oryza sativa hemoglobin 2 (hb2) gene, complete cds  
 Length=836


Score = 139 bits (75), Expect = 4e-29  
 Identities = 103/116 (89%), Gaps = 4/116 (3%)  
 Strand=Plus/Plus

Query 39 CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGGAGGCGCTGGTCTCAAGTCATGGGC 96  
 Sbjct 32 CGG-GGGGAGCGGTTCAG-CTTCAGCGAGGAGCAGGAGGCGCTTGTGCTCAAGTCGTGGGC 89  
 Query 97 CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTCTCAAGTACGTAC 152  
 Sbjct 90 CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTCTGAAGTATGTAC 145

**>emb|CU406294.1|** Oryza rufipogon (W1943) cDNA clone: ORW1943S103H20, full insert  
 sequence  
 Length=687


Score = 132 bits (71), Expect = 6e-27  
 Identities = 93/103 (91%), Gaps = 4/103 (3%)  
 Strand=Plus/Plus

Query 39 CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGGAGGCGCTGGTCTCAAGTCATGGGC 96  
 Sbjct 112 CGG-GGGGAGCGGTTCAG-CTTCAGCGAGGAGCAGGAGGCGCTTGTGCTCAAGTCGTGGGC 169  
 Query 97 CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTCT 139  
 Sbjct 170 CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTCT 212

**>emb|CT833928.1|**  Oryza sativa (indica cultivar-group) cDNA clone:OSIGCP1026D01, full insert sequence  
 Length=762

Score = 132 bits (71), Expect = 6e-27  
 Identities = 93/103 (91%), Gaps = 4/103 (3%)  
 Strand=Plus/Plus

Query 39 CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGGAGGCGCTGGTCTCAAGTCATGGGC 96  
 Sbjct 107 CGG-GGGGAGCGGTTCAG-CTTCAGCGAGGAGCAGGAGGCGCTTGTGCTCAAGTCGTGGGC 164  
 Query 97 CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTCT 139  
 Sbjct 165 CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTCT 207

**>emb|CT833927.1|**  Oryza sativa (indica cultivar-group) cDNA clone:OSIGCP1013P21, full insert sequence  
 Length=770

Score = 132 bits (71), Expect = 6e-27  
 Identities = 93/103 (91%), Gaps = 4/103 (3%)  
 Strand=Plus/Plus

Query 39 CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGC 96  
 Sbjct 107 CGG-GGGGAGCGGTTCAG-CTTCAGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCGTTGGGC 164

Query 97 CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTC 139  
 Sbjct 165 CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTC 207

>dbj|AK241096.1|  Oryza sativa Japonica Group cDNA, clone: J065076013, full insert  
 sequence  
 length=2451

Score = 132 bits (71), Expect = 6e-27  
 Identities = 93/103 (91%), Gaps = 4/103 (3%)  
 Strand=Plus/Plus

Query 39 CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGC 96  
 Sbjct 1797 CGG-GGGGAGCGGTTCAG-CTTCAGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCGTTGGGC 1854

Query 97 CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTC 139  
 Sbjct 1855 CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTC 1897


>ref|NM\_001055972.1|  Oryza sativa Japonica Group Os03g0226200 (Os03g0226200) mRNA,  
 complete cds  
 length=778

GENE ID: 4332123 Os03g0226200 | Os03g0226200 [Oryza sativa Japonica Group]  
 (10 or fewer PubMed links)

Score = 132 bits (71), Expect = 6e-27  
 Identities = 93/103 (91%), Gaps = 4/103 (3%)  
 Strand=Plus/Plus

Query 39 CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGC 96  
 Sbjct 117 CGG-GGGGAGCGGTTCAG-CTTCAGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCGTTGGGC 174

Query 97 CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTC 139  
 Sbjct 175 CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTC 217

>dbj|AK121522.1|  Oryza sativa Japonica Group cDNA clone: J033028N03, full insert  
 sequence  
 length=780

GENE ID: 4332123 Os03g0226200 | Os03g0226200 [Oryza sativa Japonica Group]  
 (10 or fewer PubMed links)

Score = 132 bits (71), Expect = 6e-27  
 Identities = 93/103 (91%), Gaps = 4/103 (3%)  
 Strand=Plus/Plus

Query 39 CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGC 96  
 Sbjct 119 CGG-GGGGAGCGGTTCAG-CTTCAGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCGTTGGGC 176


Query 97 CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTC 139  
 Sbjct 177 CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTC 219

>gb|U76031.1|OSU76031  Oryza sativa hemoglobin 2 mRNA, complete cds  
 length=786

Score = 132 bits (71), Expect = 6e-27  
 Identities = 93/103 (91%), Gaps = 4/103 (3%)  
 Strand=Plus/Plus

Query 39 CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGC 96  
 Sbjct 108 CGG-GGGGAGCGGTTCAG-CTTCAGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCGTTGGGC 165

Query 97 CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTC 139  
 Sbjct 166 CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTC 208

>ref|NM\_001056011.1|  Oryza sativa Japonica Group Os03g0233900 (Os03g0233900) mRNA,  
 complete cds  
 length=799

GENE ID: 4332166 Os03g0233900 | Os03g0233900 [Oryza sativa Japonica Group]  
 (10 or fewer PubMed links)

Score = 119 bits (64), Expect = 5e-23  
 Identities = 78/85 (92%), Gaps = 0/85 (0%)

Strand=Plus/Plus

Query 55 CTTACGCGAGGAGAAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATT 114  
 Sbjct 139 CTTACGCGAGGAGAGCAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATT 198  
 Query 115 CGCCAACCTTGGGCTCCGCTTCTTC 139  
 Sbjct 199 CGCCAATATTGCCCTCCGCTTCTTC 223

>dbj|AK064054.1|  Oryza sativa Japonica Group cDNA clone:001-125-F02, full insert  
 sequence  
 Length=799

GENE ID: 4332166 Os03g0233900 | Os03g0233900 [Oryza sativa Japonica Group]  
 (10 or fewer PubMed links)

Score = 119 bits (64), Expect = 5e-23  
 Identities = 70/85 (92%), Gaps = 0/85 (0%)  
 Strand=Plus/Plus

Query 55 CTTACGCGAGGAGAAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATT 114  
 Sbjct 139 CTTACGCGAGGAGAGCAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATT 198  
 Query 115 CGCCAACCTTGGGCTCCGCTTCTTC 139  
 Sbjct 199 CGCCAATATTGCCCTCCGCTTCTTC 223

>gb|U76030.1|OSU76030  Oryza sativa hemoglobin 1 mRNA, complete cds  
 Length=812

Score = 119 bits (64), Expect = 5e-23  
 Identities = 70/85 (92%), Gaps = 0/85 (0%)  
 Strand=Plus/Plus

Query 55 CTTACGCGAGGAGAAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATT 114  
 Sbjct 136 CTTACGCGAGGAGAGCAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATT 195  
 Query 115 CGCCAACCTTGGGCTCCGCTTCTTC 139  
 Sbjct 196 CGCCAATATTGCCCTCCGCTTCTTC 220